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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,874

DATE: 01/28/2002

TIME: 11:38:23

Input Set : N:\Crf3\RULE60\09993874.raw

Output Set: N:\CRF3\01282002\I993874.raw

1 <110> APPLICANT: Vadim R. Viviani  
 2 Yoshihiro Ohmiya  
 3 <120> TITLE OF INVENTION: Nucleic Acid Molecules Encoding Red and  
 4 Green Emitting Luciferases  
 5 <130> FILE REFERENCE: 2799.1001-001  
 6 <140> CURRENT APPLICATION NUMBER: US/09/993,874  
 7 <141> CURRENT FILING DATE: 2001-11-14  
 8 <150> PRIOR APPLICATION NUMBER: 09/516,958  
 9 <151> PRIOR FILING DATE: 2000-03-01  
 10 <150> PRIOR APPLICATION NUMBER: IT 5339  
 11 <151> PRIOR FILING DATE: 1998-09-02  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 13 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 1765  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Phrixothrix vivianii  
 19 <220> FEATURE:  
 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (26)...(1660)  
 22 <400> SEQUENCE: 1

23	tcagtgaag actttaggga tcaaa atg gaa gaa gaa aac att agg cat gga	52
24	Met Glu Glu Glu Asn Ile Arg His Gly	
25	1 5	
26	gag cgt cct cgt gat ata gtc cat cct ggc tcg gca gga caa caa tta	100
27	Glu Arg Pro Arg Asp Ile Val His Pro Gly Ser Ala Gly Gln Gln Leu	
28	10 15 20 25	
29	tac caa tca ttg tat aaa ttt gca tct ttt cct gaa gca ata atc gat	148
30	Tyr Gln Ser Leu Tyr Lys Phe Ala Ser Phe Pro Glu Ala Ile Ile Asp	
31	30 35 40	
32	gct cat aca aat gaa gta ata tca tat gct caa ata ttt gaa acc agc	196
33	Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile Phe Glu Thr Ser	
34	45 50 55	
35	tgc cgc tta gct gtt agt ata gaa caa tat ggc ttg aat gaa aac aat	244
36	Cys Arg Leu Ala Val Ser Ile Glu Gln Tyr Gly Leu Asn Glu Asn Asn	
37	60 65 70	
38	gtt gtg ggt gta tgc agt gaa aac aat ata aac ttt ttt aat cct gtc	292
39	Val Val Gly Val Cys Ser Glu Asn Asn Ile Asn Phe Phe Asn Pro Val	
40	75 80 85	
41	ctt gct gct tta tac tta gga ata cca gta gca aca tca aat gat atg	340
42	Leu Ala Ala Leu Tyr Leu Gly Ile Pro Val Ala Thr Ser Asn Asp Met	
43	90 95 100 105	
44	tac aca gat gga gag tta act ggt cat ttg aat ata tca aaa cca act	388

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45	Tyr	Thr	Asp	Gly	Glu	Leu	Thr	Gly	His	Leu	Asn	Ile	Ser	Lys	Pro	Thr	
46					110					115					120		
47	atc	atg	ttt	agt	tca	aag	aaa	gca	ctc	ccg	ctt	att	ctg	aga	gta	cag	436
48	Ile	Met	Phe	Ser	Lys	Lys	Ala	Leu	Pro	Leu	Ile	Leu	Arg	Val	Gln		
49				125					130					135			
50	caa	aat	cta	agt	ttc	att	aaa	aaa	gtc	gta	gtt	atc	gat	agc	atg	tac	484
51	Gln	Asn	Leu	Ser	Phe	Ile	Lys	Lys	Val	Val	Val	Ile	Asp	Ser	Met	Tyr	
52			140						145					150			
53	gac	att	aat	ggc	gtt	gaa	tgc	gta	tct	acc	ttt	gtt	gca	cgt	tat	act	532
54	Asp	Ile	Asn	Gly	Val	Glu	Cys	Val	Ser	Thr	Phe	Val	Ala	Arg	Tyr	Thr	
55			155						160					165			
56	gac	cac	acc	ttt	gat	cca	ttg	tca	ttt	aca	cca	aaa	gat	ttt	gat	ccc	580
57	Asp	His	Thr	Phe	Asp	Pro	Leu	Ser	Phe	Thr	Pro	Lys	Asp	Phe	Asp	Pro	
58	170					175					180					185	
59	ctt	gaa	aaa	atc	gca	tta	att	atg	tca	tca	tct	gga	aca	act	gga	ttg	628
60	Leu	Glu	Lys	Ile	Ala	Leu	Ile	Met	Ser	Ser	Ser	Gly	Thr	Thr	Gly	Leu	
61					190						195				200		
62	cct	aag	ggt	gta	gta	ctg	agc	cat	aga	agt	cta	act	ata	aga	ttc	gtt	676
63	Pro	Lys	Gly	Val	Val	Leu	Ser	His	Arg	Ser	Leu	Thr	Ile	Arg	Phe	Val	
64				205					210					215			
65	cat	agc	agg	gat	ccc	att	tat	ggc	act	cgt	acg	gtt	cca	caa	aca	tca	724
66	His	Ser	Arg	Asp	Pro	Ile	Tyr	Gly	Thr	Arg	Thr	Val	Pro	Gln	Thr	Ser	
67			220					225					230				
68	att	ctt	tcc	tta	gta	ccg	ttc	cat	cat	gcc	ttt	gga	atg	ttt	act	aca	772
69	Ile	Leu	Ser	Leu	Val	Pro	Phe	His	His	Ala	Phe	Gly	Met	Phe	Thr	Thr	
70		235					240					245					
71	tta	tct	tac	ttt	gta	gta	gga	ctt	aag	gtt	gta	atg	ttg	aag	aaa	ttt	820
72	Leu	Ser	Tyr	Phe	Val	Val	Gly	Leu	Lys	Val	Val	Met	Leu	Lys	Lys	Phe	
73	250					255					260					265	
74	gag	ggc	gca	ctt	ttc	tta	aaa	acc	ata	cag	aat	tac	aaa	atc	ccc	act	868
75	Glu	Gly	Ala	Leu	Phe	Leu	Lys	Thr	Ile	Gln	Asn	Tyr	Lys	Ile	Pro	Thr	
76				270						275					280		
77	att	gta	gtg	gcc	cct	cca	gtt	atg	gtg	ttt	ttg	gct	aaa	agc	cca	tta	916
78	Ile	Val	Val	Ala	Pro	Pro	Val	Met	Val	Phe	Leu	Ala	Lys	Ser	Pro	Leu	
79				285					290					295			
80	gtc	gat	caa	tac	gat	tta	tcg	agc	tta	acg	gaa	gtt	gct	act	gga	gga	964
81	Val	Asp	Gln	Tyr	Asp	Leu	Ser	Ser	Leu	Thr	Glu	Val	Ala	Thr	Gly	Gly	
82			300					305					310				
83	gct	cct	tta	gga	aaa	gat	gtc	gca	gaa	gca	gta	gca	aag	agg	ttg	aaa	1012
84	Ala	Pro	Leu	Gly	Lys	Asp	Val	Ala	Glu	Ala	Val	Ala	Lys	Arg	Leu	Lys	
85		315					320					325					
86	tta	cct	gga	atc	ata	caa	gga	tat	gga	tta	act	gaa	act	tgc	tgc	gct	1060
87	Leu	Pro	Gly	Ile	Ile	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Cys	Cys	Ala	
88	330					335					340					345	
89	gta	atg	att	acc	cct	cat	aat	gct	gtg	aaa	aca	ggt	tca	act	gga	aga	1108
90	Val	Met	Ile	Thr	Pro	His	Asn	Ala	Val	Lys	Thr	Gly	Ser	Thr	Gly	Arg	
91				350						355					360		
92	ccc	ttg	cca	tac	att	aaa	gct	aaa	gtt	tta	gat	aac	gct	act	ggg	aag	1156
93	Pro	Leu	Pro	Tyr	Ile	Lys	Ala	Lys	Val	Leu	Asp	Asn	Ala	Thr	Gly	Lys	

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94          365          370          375
95  gcg cta gga cca gga gaa aga ggc gaa ata tgc ttt caa agt gaa atg 1204
96  Ala Leu Gly Pro Gly Glu Arg Gly Glu Ile Cys Phe Gln Ser Glu Met
97          380          385          390
98  att atg aaa gga tat tac aac aat ccg gaa gca act att gat act att 1252
99  Ile Met Lys Gly Tyr Tyr Asn Asn Pro Glu Ala Thr Ile Asp Thr Ile
100          395          400          405
101  gac aaa gat ggt tgg ctt cat tct gga gat att gga tat tac gac gaa 1300
102  Asp Lys Asp Gly Trp Leu His Ser Gly Asp Ile Gly Tyr Tyr Asp Glu
103  410          415          420          425
104  gat gga aat ttc ttt ata gtt gat cga ttg aaa gaa ctt att aaa tac 1348
105  Asp Gly Asn Phe Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr
106          430          435          440
107  aag gga tat cag gtt gcg cct gct gaa ctg gaa aat ctg ctt tta caa 1396
108  Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Asn Leu Leu Leu Gln
109          445          450          455
110  cat cca agt att gct gat gcg ggt gtt act gga gtt ccg gac gaa ttt 1444
111  His Pro Ser Ile Ala Asp Ala Gly Val Thr Gly Val Pro Asp Glu Phe
112          460          465          470
113  ggt gga caa tta cct gct gct tgt gtt gtg tta gaa tct ggc aag acg 1492
114  Gly Gly Gln Leu Pro Ala Ala Cys Val Val Leu Glu Ser Gly Lys Thr
115          475          480          485
116  ctg act gaa aag gaa gtt caa gat ttt att gca gca caa gtc act cca 1540
117  Leu Thr Glu Lys Glu Val Gln Asp Phe Ile Ala Ala Gln Val Thr Pro
118  490          495          500          505
119  aca aag cat ctt cga ggc ggt gtc gta ttt gta gac agt att ccg aaa 1588
120  Thr Lys His Leu Arg Gly Gly Val Val Phe Val Asp Ser Ile Pro Lys
121          510          515          520
122  ggc cct act gga aaa ctc atc aga aag gag ctc cga gaa ata ttt gcc 1636
123  Gly Pro Thr Gly Lys Leu Ile Arg Lys Glu Leu Arg Glu Ile Phe Ala
124          525          530          535
125  cag cga gca cca aaa tca aaa tta taagttcaat gtattgcttt agttctaaaa 1690
126  Gln Arg Ala Pro Lys Ser Lys Leu
127          540          545
128  tgtatataaaa caagtttttag aacctaatac attcattcaa atactaaaca aaaaaaaaaa 1750
129  aaaaaaaaaa aaaaaa 1765
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 545
133 <212> TYPE: PRT
134 <213> ORGANISM: Phrixothrix vivianii
135 <400> SEQUENCE: 2
136  Met Glu Glu Glu Asn Ile Arg His Gly Glu Arg Pro Arg Asp Ile Val
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138  His Pro Gly Ser Ala Gly Gln Gln Leu Tyr Gln Ser Leu Tyr Lys Phe
139          20          25          30
140  Ala Ser Phe Pro Glu Ala Ile Ile Asp Ala His Thr Asn Glu Val Ile
141          35          40          45
142  Ser Tyr Ala Gln Ile Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Ile
143          50          55          60

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144   Glu Gln Tyr Gly Leu Asn Glu Asn Asn Val Val Gly Val Cys Ser Glu
145   65                               70                               75                               80
146   Asn Asn Ile Asn Phe Phe Asn Pro Val Leu Ala Ala Leu Tyr Leu Gly
147                               85                               90                               95
148   Ile Pro Val Ala Thr Ser Asn Asp Met Tyr Thr Asp Gly Glu Leu Thr
149                               100                              105                              110
150   Gly His Leu Asn Ile Ser Lys Pro Thr Ile Met Phe Ser Ser Lys Lys
151                               115                              120                              125
152   Ala Leu Pro Leu Ile Leu Arg Val Gln Gln Asn Leu Ser Phe Ile Lys
153                               130                              135                              140
154   Lys Val Val Val Ile Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys
155   145                               150                               155                               160
156   Val Ser Thr Phe Val Ala Arg Tyr Thr Asp His Thr Phe Asp Pro Leu
157                               165                               170                               175
158   Ser Phe Thr Pro Lys Asp Phe Asp Pro Leu Glu Lys Ile Ala Leu Ile
159                               180                              185                              190
160   Met Ser Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Val Leu Ser
161                               195                              200                              205
162   His Arg Ser Leu Thr Ile Arg Phe Val His Ser Arg Asp Pro Ile Tyr
163                               210                              215                              220
164   Gly Thr Arg Thr Val Pro Gln Thr Ser Ile Leu Ser Leu Val Pro Phe
165   225                               230                               235                               240
166   His His Ala Phe Gly Met Phe Thr Thr Leu Ser Tyr Phe Val Val Gly
167                               245                               250                               255
168   Leu Lys Val Val Met Leu Lys Lys Phe Glu Gly Ala Leu Phe Leu Lys
169                               260                              265                              270
170   Thr Ile Gln Asn Tyr Lys Ile Pro Thr Ile Val Val Ala Pro Pro Val
171                               275                              280                              285
172   Met Val Phe Leu Ala Lys Ser Pro Leu Val Asp Gln Tyr Asp Leu Ser
173   290                               295                               300
174   Ser Leu Thr Glu Val Ala Thr Gly Gly Ala Pro Leu Gly Lys Asp Val
175   305                               310                               315                               320
176   Ala Glu Ala Val Ala Lys Arg Leu Lys Leu Pro Gly Ile Ile Gln Gly
177                               325                               330                               335
178   Tyr Gly Leu Thr Glu Thr Cys Cys Ala Val Met Ile Thr Pro His Asn
179                               340                              345                              350
180   Ala Val Lys Thr Gly Ser Thr Gly Arg Pro Leu Pro Tyr Ile Lys Ala
181   355                               360                               365
182   Lys Val Leu Asp Asn Ala Thr Gly Lys Ala Leu Gly Pro Gly Glu Arg
183   370                               375                               380
184   Gly Glu Ile Cys Phe Gln Ser Glu Met Ile Met Lys Gly Tyr Tyr Asn
185   385                               390                               395                               400
186   Asn Pro Glu Ala Thr Ile Asp Thr Ile Asp Lys Asp Gly Trp Leu His
187                               405                               410                               415
188   Ser Gly Asp Ile Gly Tyr Tyr Asp Glu Asp Gly Asn Phe Phe Ile Val
189                               420                              425                              430
190   Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro
191   435                               440                               445
192   Ala Glu Leu Glu Asn Leu Leu Leu Gln His Pro Ser Ile Ala Asp Ala

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193          450          455          460
194 Gly Val Thr Gly Val Pro Asp Glu Phe Gly Gly Gln Leu Pro Ala Ala
195 465          470          475          480
196 Cys Val Val Leu Glu Ser Gly Lys Thr Leu Thr Glu Lys Glu Val Gln
197          485          490          495
198 Asp Phe Ile Ala Ala Gln Val Thr Pro Thr Lys His Leu Arg Gly Gly
199          500          505          510
200 Val Val Phe Val Asp Ser Ile Pro Lys Gly Pro Thr Gly Lys Leu Ile
201          515          520          525
202 Arg Lys Glu Leu Arg Glu Ile Phe Ala Gln Arg Ala Pro Lys Ser Lys
203          530          535          540
204 Leu
205 545
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1760
209 <212> TYPE: DNA
210 <213> ORGANISM: Phrixothrix hirtus
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (41)...(1678)
214 <400> SEQUENCE: 3
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216                               Met Glu Glu Glu Asn
217                               1 5
218 gtt gtg aat gga gat cgt cct cgt gat cta gtt ttt cct ggc aca gca 103
219 Val Val Asn Gly Asp Arg Pro Arg Asp Leu Val Phe Pro Gly Thr Ala
220          10          15          20
221 gga cta caa tta tat caa tca tta tat aaa tat tca tat att act gac 151
222 Gly Leu Gln Leu Tyr Gln Ser Leu Tyr Lys Tyr Ser Tyr Ile Thr Asp
223          25          30          35
224 gga ata atc gat gcc cat acc aat gaa gta ata tca tat gct caa ata 199
225 Gly Ile Ile Asp Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile
226          40          45          50
227 ttt gaa acc agc tgc cgc ttg gca gtt agt cta gaa aaa tat ggc ttg 247
228 Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Leu Glu Lys Tyr Gly Leu
229          55          60          65
230 gat cat aac aat gtt gtg gca ata tgc agt gaa aac aac ata cac ttt 295
231 Asp His Asn Asn Val Val Ala Ile Cys Ser Glu Asn Asn Ile His Phe
232          70          75          80          85
233 ttt ggc cct tta att gct gct tta tac caa gga ata cca atg gca aca 343
234 Phe Gly Pro Leu Ile Ala Ala Leu Tyr Gln Gly Ile Pro Met Ala Thr
235          90          95          100
236 tca aat gat atg tac aca gaa agg gag atg att ggc cat ttg aat ata 391
237 Ser Asn Asp Met Tyr Thr Glu Arg Glu Met Ile Gly His Leu Asn Ile
238          105          110          115
239 tcg aaa cca tgc ctt atg ttt tgt tca aag aaa tca ctc cca ttt att 439
240 Ser Lys Pro Cys Leu Met Phe Cys Ser Lys Lys Ser Leu Pro Phe Ile
241          120          125          130
242 ctg aaa gta caa aaa cat cta gat ttc ctt aaa aga gtc ata gtc att 487

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**VERIFICATION SUMMARY**

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